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Detection of MRSA and MSSA CC398 isolates in cystic fibrosis patients of a Spanish Hospital

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Background

Staphylococcus aureus is one of the most prevalent pathogens in cystic fibrosis (CF).

Methicillin resistant *S. aureus* (MRSA) presence is increasingly reported, as well as the emergence of livestock-associated (LA)-MRSA lineage in CF patients.

The objective of this study was to determine the resistance phenotype/genotype, the virulence content, and molecular typing of *S. aureus* isolates from CF infections

Methods

40 *S. aureus* isolates were obtained from CF patients of a Spanish hospital during January-April 2022 (one isolate per patient).

The phenotype and genotype of antimicrobial resistance was evaluated by Microscan and PCR-sequencing.

The presence of *lukS/lukF*-PV, *eta*, *etb*, and *tst* genes was determined by PCR.

Molecular typing (*agr*-, *spa*-typing) was studied by PCR-sequencing, and the Immune Evasion Cluster (IEC) genes were analysed by PCR.

Results

7 isolates were MRSA, being all of them multi-resistant isolates.

The 55% of MSSA isolates were multi-resistant.

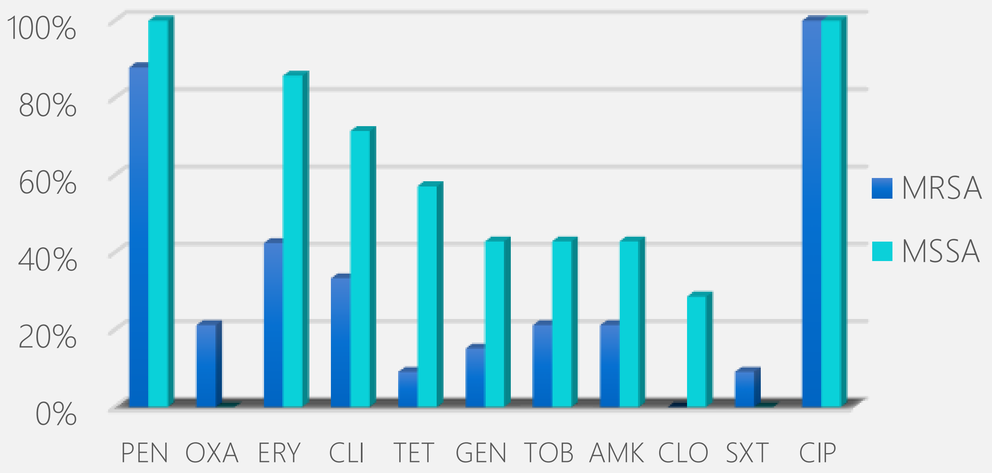

Figure 1. Frequency of antimicrobial resistance of the 40 *S. aureus* isolates.
PEN, penicillin; OXA, oxacillin; ERY, erythromycin; CLI, clindamycin; TET, tetracycline; GEN, gentamicin; TOB, tobramycin; AMK, amikacin; CIP, ciprofloxacin; SXT, trimethoprim-sulfamethoxazole

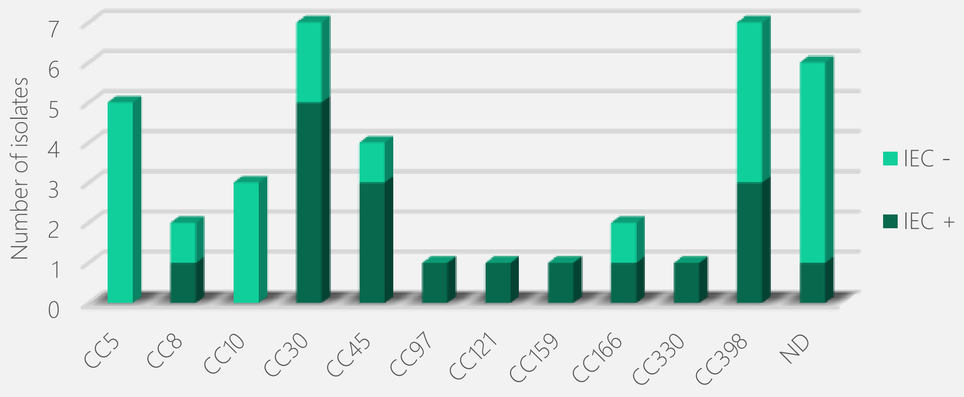

Figure 2. Distribution of IEC according to clonal complexes.

7 CC398 isolates were detected:
- 1 MRSA-t011-IEC negative
- 6 MSSA-t011-t034-t108-t571

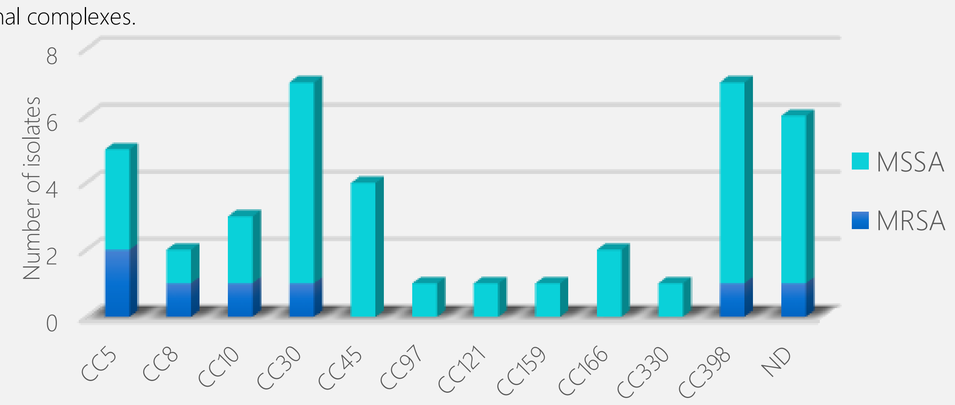

Figure 3. Distribution of MRSA a MSSA according to clonal complexes.

Table 1. Characteristics of the 7 CC398 isolates of this study

	spa-type	IEC	Resistance phenotype	Resistance genotype
MRSA	t011 (1)	-	PEN, OXA, ERY, CLI, TET, GEN, TOB, AMK, CLO, CIP	*blaZ*, *mecA*, *tet*(K), *tet*(M), *erm*(A), *aac*(6')-Ie-*aph*-(2'')-Ia, *ant*(4')-Ia, *aph*(3')-III
MSSA	t011 (1)	-	PEN, ERY, CLI, TOB, AMK, CIP	*blaZ*, *erm*(A), *vga*(A), *aac*(6')-Ie-*aph*-(2'')-Ia
	t034 (1)	-	PEN, TET, GEN, TOB, AMK, CIP	*blaZ*, *tet*(M), *ant*(4')-Ia, *aph*(3')-III
	t108 (2)	B[1]/-[1]	PEN, ERY, CLI[1], TET[1], CIP, SXT[1]	*blaZ*, *tet*(M)[1], *mrs*(A)[1], *mph*(C)[1]
	t571 (2)	F	PEN, ERY, CLI[Ind], CIP	*blaZ*, *erm*(T)

A number in superscript reflects when not all isolates of the group have the referred characteristic
PEN, penicillin; OXA, oxacillin; ERY, erythromycin; CLI, clindamycin; TET, tetracycline; GEN, gentamicin; TOB, tobramycin; AMK, amikacin; CIP, ciprofloxacin; SXT, trimethoprim-sulfamethoxazole

The MRSA isolate belonged to CC398-t011-IEC negative (animal-clade), and it was multi-resistant.

The two t571-IEC-positive-MSSA isolates presented the gene *erm*(T) (human-clade).

Among the 33 non-CC398 isolates, 12 of them lacked the *scn* gene (36%), of the lineages CC5, CC8, CC10, CC30, CC45, CC166

Table 2 Percentage of occurrence of virulence genes

Virulence gene	Clonal complaxes
tst (33%)	CC5, CC10, CC30, CC45, CC166, CC330, CC398
eta (5%)	CC159, CC330

- The *tst* gene was detected in 13 isolates being all MSSA. The *eta* gene was detected in 2 MSSA-IEC B isolates
- In one isolate (MSSA-t130-CC330) *tst* and *eta* genes were detected at the same time.
- None isolate harboured PVL gene.

Conclusions

1. MRSA and MSSA isolates of lineage CC398 were found in CF patients showing characteristic of both human and animal clades.
2. Non CC398-IEC negative were identified.
3. The emergence of LA clonal lineages in CF patients should be further analysed and monitored.

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